

### In the Specification:

Replace the alignment starting on page 10, line 14 with the following alignment.

gi 547724	INTERFERON ALPHA PRECURSOR (IFN-ALPHA)	(SEQ ID NO:11)
gi 585317	INTERFERON DELTA-1 PRECURSOR	(SEQ ID NO:12)
gi 124502	INTERFERON OMEGA-2 PRECURSOR (INTERFERON ALPHA-II-2)	(SEQ ID NO:13)
gi 400061	INTERFERON OMEGA-1 PRECURSOR (INTERFERON ALPHA-II-1)	(SEQ ID NO:14)

Sequence alignment of NOV1a and several interferon genes. The alignment shows a highly conserved region from position 70 to 110. NOV1a is at the top, followed by gi|547724, gi|585317, gi|124502, and gi|400061. A consensus sequence is shown at the bottom. Positions 70, 80, 90, 100, and 110 are marked above the alignment. A vertical bar at position 80 indicates a conserved residue.

Replace the alignment starting on page 11, line 8 with the following alignment.

gi|3318960|pdb|1AU1|A Chain A, Human Interferon-Beta Crystal Structure (SEQ\_ID\_NO:16)  
gi|2624437|pdb|1RH2|A Chain A, Recombinant Human Interferon-Alpha 2b (SEQ\_ID\_NO:17)  
gi|124432|INTERFERON ALPHA-1 PRECURSOR (SEQ\_ID\_NO:18)  
gi|2147609|interferon-omega20 - rabbit (SEQ\_ID\_NO:19)  
Consensus (SEQ\_ID\_NO:20)

10 20 30 40 50 60  
 NOV1a ..... DLPKAQVVISALHMHQQIFSLFLHKGLSDAWNRAFLDKLQTGFHQQL  
 gi|3318960|pdb| NFDIPEEIKQLQQFKQEDAALTLYEMLQNTPAIYPRODSSSTCWNEVLEVNLLANVYHQIN  
 gi|2624437|pdb| DFGFPGEEFG-NQFOQAEITIPVLEHEMHQQTIFNLFSKRDSSAAWDETLTLDKFTYELMQQLN  
 gi|124432|INTER| DFGFPGEEKVDAQQIKKAQAIYFVLSLTTQOQINPFTSKDSSAAWNATLSDFCNDLHQQLQ  
 gi|2147609|inte| DFQFPREVVNGSQFKQNOTVSVLHEMHQQTIFNLTSARSSAAWNNTLLEELHTALHQQLQ  
 Consensus F P E Q K L E M Q Q I F F S S A W N T L Q Q Q L

Sequence alignment of NOV1a and its orthologs. The alignment shows the amino acid sequence of NOV1a (top) and its orthologs (gi|3318960, gi|2624437, gi|124432, gi|2147609) in the PDB. The alignment is color-coded by residue type: hydrophobic (black), polar (white), and charged (grey). A scale bar at the top indicates positions 70, 80, 90, 100, and 110. A consensus sequence is shown at the bottom.

Amend the paragraph starting on page 20, line 12 as follows.

This same alignment between KIAA1246 (SEQ ID NO:27) and NOV2 (identified as

AF038458A) is shown below.

Replace the alignment starting on page 21, line 1 with the following alignment.

KIAA\_predicted -- MET L L G G L L A F G M A -- . . . . F A V V D A C P K Y C V C Q N L S E S L G T L C P S K G L L F V P P D D D R R  
AF038458\_A M A I L P L L L C L L P L A P A S S F P Q S A T P S P C P R R C R C Q T Q S L P L S V L C P G A G L L F V P P S L D R R

KIAA\_predicted T V E L R I G G N F I I H I S H Q D F A N M T G L V D L T L S R N T I S H I Q P F S F L D I E S L E S L H L D S M R L P  
RICK\_AF038458\_A A A E L R I A D M F I A S V R R D L A N M T G L E H I S L S R N T I R H Y A A G A F A D L R A L H L D G N E L T

KIAA\_predicted S L G E D T L R G L V N L Q H L I V N N N Q L G C G I A D E A F E D F L L T L E D D L D S Y V N N L H G L P W D S W R E M V  
AF038458 A S L G E G Q L R G L V N L R H L I L S N N Q L A A L A G A L D D C A T L E D D L D S Y V N N L E Q L P W E A L G F G

KIAA\_predicted\_HNLHQQLSLDHNLLDHITAEGTFADLQQLKLRALDLTSNRLQKLPEDFTFARSQASALTATPFAA\_AF038458\_A\_HNVTLLGLDHNLLASVPGAGAFSRLHKLARLDMTSNRETTIIPPDFTFSELPLLARPRGSPAS

KIAA\_predicted PLSFSFGGNPLHCNCELWLRRLERDDDETCGSPGGLKGRYFWHREEEFVCEPFLITQ  
AF038458 A ALVLAFGGNPLHCNCELWLRRLAREDDLEACASPPALGGRYFWAUGEEE FVCEPFWVTH

KIAA\_predicted H I H K L L W L E G Q A A T L K C K A T G D P S F L I H W W A F D D R I V G M S S R T A V M D N G T L D I F I L T T S Q D  
AF038458 A R S P P L A W T A G R P A A L L R C R A V G D P E F P R V R W W S P O G R L L G M S S R A R A F P N G T L E L L V T E P G D

KIAA\_predicted SGAAFTCIAANAAAGEATAMWEVSILVQLF--HLSNSTSRTAPPKSRLSDITGSSKTERRGGGG  
AF038458 A GGIIFTCIAANAAAGEATAAWEVLTWGGPPPPPOLANSTSCDPP---RDGDPDALTPPSAASAS

KIAA\_predicted SGGGEPPKSFPERAWLWSLEVTTT SALWKWSVSKSAFRVKMVOQVNCSDDDEVLLVYRMIPA  
AF038458 A AKVADTG-PPTDRGIVQVTEHGATAALWQWPDQRPIPGIRMYQIIVYNSSADDILVYRMIPA

KIAA\_predicted S N K A F V V N N L V S G T G V D L C V L A M M W D D I T A T T L T A T N I V G C A Q F F T K A D Y P Q C Q S M H S Q I L G  
AF038458 A E S R S F I L L T D L A S C R T V D L C V L A M V E D S A T G L T A T R P V G C A R F S T E P A L R P Q G A P H A P F L G

KIAA\_predicted G T M I I L V R G G I I V A R L L V F I V I L M W R Y K W C N H E A P - S K M A A A N S N W Y S Q T N G A Q P P P F S S  
AF038458 A G T M I I K A L G G V I V A S V L V F I F V L L M W R Y K W H G G O P P G K A K I P A P V S S W C S Q T N G A L G P T F T -

**KIAA\_predicted** KP3LDRLMGAFASLDLKSQRKEELLDsRTFAGRGAGTSARGHHSDREPLLGPPAARARSL  
AF038458 A-----

KIAA\_predicted DLVGARGTFGSSEWVME S T V  
AE022452 A

Digitized by srujanika@gmail.com

Please replace the current sequence listing with the one enclosed.